09/772,284 245.549

WEST

Freeform Search

Database: US Patents Full-Text Database; US Pre-Grant Publication Full-Text Database; JPO Abstracts Database; EPO Abstracts Database; Derwent World Patents Index; IBM Technical Disclosure Bulletins

Term: L7 and in vivo

Display: 10 **Documents in Display Format:** - **Starting with Number** 1

Generate: ○ Hit List ◉ Hit Count ○ Side by Side ○ Image

Search | Clear | Help | Logout | Interrupt

Main Menu | Show S Numbers | Edit S Numbers | Preferences | Cases

Search History

DATE: Wednesday, July 02, 2003 Printable Copy Create Case

Set Name side by side	Query	Hit Count	Set Name result set
DB=USPT,JPAB,EPAB,DWPI; PLUR=YES; OP=ADJ			
L8	L7 and in vivo	10	L8
L7	l1 and (one insert or single insert or a DNA insert)	29	L7
L6	l1 and single DNA molecule insert	0	L6
L5	homolog$3 near5 recombin$3 near5 (one insert or single insert or single DNA molecule insert)	0	L5
L4	homolog$3 near5 recombn$3 near5 (one insert or single insert or single DNA molecule insert)	0	L4
L3	homolog$3 near5 recombin$3 near5(one insert or single insert) near5 one vector	0	L3
L2	L1 and one insert and one vector and in vivo	1	L2
L1	homolog$3 near5 recombin$3	2289	L1

END OF SEARCH HISTORY

Generate Collection | Print

Search Results - Record(s) 1 through 10 of 10 returned.

☐ 1. 6562596 . 06 Oct 93; 13 May 03. Tissue inhibitor of metalloproteinase type three (TIMP-3) composition and methods. Silbiger; Scott M., et al. 435/69.2; 435/252.3 435/320.1 435/325 435/69.1 536/23.5. C12P021/02.

☐ 2. 6410271 . 23 Jun 00; 25 Jun 02. Generation of highly diverse library of expression vectors via homologous recombination in yeast. Zhu; Li, et al. 435/69.7; 435/483 435/69.1 435/7.1 435/71.1. C12P021/04 C12P021/06 C12N015/74 C12N033/53.

☐ 3. 6410246 . 23 Jun 00; 25 Jun 02. Highly diverse library of yeast expression vectors. Zhu; Li, et al. 435/7.1; 435/320.1 435/7.31 536/23.4 536/23.53. G01N033/53.

☐ 4. 6406863 . 23 Jun 00; 18 Jun 02. High throughput generation and screening of fully human antibody repertoire in yeast. Zhu; Li, et al. 435/7.1; 435/29 435/69.7 435/7.8 435/71.1. G01N033/53 C12Q001/02 C12P021/04.

☐ 5. 6379943 . 05 Mar 99; 30 Apr 02. High-efficiency Cre/loxp based system for construction of adenovirus vectors. Graham; Frank L., et al. 435/235.1; 435/320.1 435/325 435/366 435/369. C12N005/10 C12N007/01 C12N015/861.

☐ 6. 6270989 . 17 Mar 95; 07 Aug 01. Protein production and delivery. Treco; Douglas A., et al. 435/69.1; 435/208 435/346 435/367 435/371 435/372.3 435/463 435/69.4 435/69.51 435/69.6 435/69.7 530/350 536/23.4 536/23.51 536/24.1. C12P021/02.

☐ 7. 5968502 . 26 May 95; 19 Oct 99. Protein production and protein delivery. Treco; Douglas, et al. 424/93.21; 424/425 435/320.1 435/325 435/455 435/69.1 536/23.1. A01N063/00.

☑ 8. 5935824 . 31 Jan 96; 10 Aug 99. Protein expression system. Sgarlato; Gregory D.. 435/69.7; 435/69.8 530/350 536/23.4. C07K019/00 C12N015/62.

☑ 9. 5733761 . 26 May 95; 31 Mar 98. Protein production and protein delivery. Treco; Douglas, et al. 435/463; 435/69.4 536/23.51 536/24.1. C12N015/00 C12P021/00 C07H021/04.

☑ 10. 5641670 . 13 May 94; 24 Jun 97. Protein production and protein delivery. Treco; Douglas A., et al. 435/325; 435/254.11 435/320.1 435/326 435/366 435/367 435/371 435/372 435/372.2 435/372.3 435/419. C12N005/06 C12N005/08 C12N015/85.

Generate Collection | Print

Generate Collection

L8: Entry 9 of 10 File: USPT Mar 31, 1998

DOCUMENT-IDENTIFIER: US 5733761 A
TITLE: Protein production and protein delivery

Detailed Description Text (52):
Gene targeting occurs when transfecting DNA either integrates into or partially replaces chromosomal DNA sequences through a homologous recombinant event. While such events can occur in the course of any given transfection experiment, they are usually masked by a vast excess of events in which plasmid DNA integrates by nonhomologous, or illegitimate, recombination.

Detailed Description Text (105):
Plasmid pXEPO-10 is designed to replace exon 1 of hEPO with exon 1 of hGH by gene targeting to the endogenous hEPO gene on human chromosome 7. Plasmid pXEPO-10 is constructed as follows. First, the intermediate plasmid pT163 is constructed by inserting the 6 kb HindIII-BamHI fragment (see Example 1f) lying upstream of the hEPO coding region into HindIII-BamHI digested pBluescriptII SK+ (Stratagene, LaJolla, Calif.). The product of this ligation is digested with XhoI and HindIII and ligated to the 1.1 kb HindIII-XhoI fragment from pMClneoPolyA [Thomas, K. R. and Capecchi, M. R. Cell 51: 503-512 (1987) available from Strategene, LaJolla, Calif.] to create pT163. Oligonucleotides 13.1-13.4 are utilized in polymerase chain reactions to generate a fusion fragment in which the mouse metallothionein 1 (mMT-I) promoter-hGH exon 1 sequences are additionally fused to hEPO intron 1 sequences. First, oligonucleotides 13.1 and 13.2 are used to amplify the approximately 0.73 kb mMT-I promoter-hGH exon 1 fragment from pXGH5 (FIG. 1). Next, oligonucleotides 13.3 and 13.4 are used to amplify the approximately 0.57 kb fragment comprised predominantly of hEPO intron 1 from human genomic DNA. Finally, the two amplified fragments are mixed and further amplified with oligonucleotides 13.1 and 13.4 to generate the final fusion fragment (fusion fragment 3) flanked by a SalI site at the 5' side of the mMT-I moiety and an XhoI site at the 3' side of the hEPO intron 1 sequence. Fusion fragment 3 is digested with XhoI and SalI and ligated to XhoI digested pT163. The ligation mixture is transformed into E. coli and a clone containing a single insert of fusion fragment 3 in which the XhoI site is regenerated at the 3' side of hEPO intron 1 sequences is identified and designated pXEPO-10. ##STR1## The non-boldface region of oligo 13.1 is identical to the mMT-I promoter, with the natural KpnI site as its 5' boundary. The boldface type denotes a SalI site tail to convert the 5' boundary to a SalI site. The boldface region of oligos 13.2 and 13.3 denote hGH sequences, while the non-boldface regions are intron 1 sequences from the hEPO gene. The non-boldface region of oligo 13.4 is identical to last 25 bases of hEPO intron 1. The boldface region includes an XhoI site tail to convert the 3' boundary of the amplified fragment to an XhoI site.

Detailed Description Text (106):
Plasmid pXEPO-11 is designed to place, by gene targeting, the mMT-I promoter and exon 1 of hGH upstream of the hEPO structural gene and promoter region at the endogenous hEPO locus on human chromosome 7. Plasmid pXEPO-11 is constructed as follows. Oligonucleotides 13.1 and 13.5-13.7 are utilized in polymerase chain reactions to generate a fusion fragment in which the mouse metallothionein I (mMT-I) promoter-hGH exon 1 sequences are additionally fused to hEPO sequences from -1 to -630 relative to the hEPO coding region. First, oligonucleotides 13.1 and 13.5 are used to amplify the approximately 0.73 kb mMT-I promoter-hGH exon 1 fragment from pXGH5 (FIG. 1). Next, oligonucleotides 13.6 and 13.7 are used to amplify, from human genomic DNA, the approximately 0.62 kb fragment comprised predominantly of hEPO sequences from -1 to -620 relative to the hEPO coding region. Both oligos 13.5 and 13.6 contain a 10 bp linker sequence located at the hGH intron 1-hEPO promoter region, which corresponds to the natural hEPO intron 1 splice donor site. Finally, the two amplified fragments are mixed and further amplified with oligonucleotides 13.1 and 13.7 to generate the final fusion fragment (fusion fragment 6) flanked by a SalI site at the 5' side of the mMT-I

moiety and an XhoI site at the 3' side of the hEPO promoter region. Fusion fragment 6 is digested with XhoI and SalI and ligated to XhoI digested pT163. The ligation mixture is transformed into E. coli and a clone containing a single insert of fusion fragment 6 in which the XhoI site is regenerated at the 3' side of hEPO promoter sequences is identified and designated pXEPO-11. ##STR2## The boldface regions of oligos 13.5 and 13.6 denote hGH sequences. The italicized regions correspond to the first 10 base pairs of hEPO intron 1. The remainder of the oligos correspond to hEPO sequences from -620 to -597 relative to the hEPO coding region. The non-boldface region of oligo 13.7 is identical to bases -1 to -24 relative to the hEPO coding region. The boldface region includes an XhoI site tail to convert the 3' boundary of the amplified fragment to an XhoI site.

Detailed Description Text (110):
First, the intermediate plasmid pT164 is constructed by inserting the 6 kb HindIII-BamHI fragment (Example 1f) lying upstream of the hEPO coding region into HindIII-BamHI digested pBluescriptII SK+ (Stratagene, LaJolla, Calif.). Plasmid pMC1neoPolyA [Thomas, K. R. and Capecchi, M. R. Cell 51:503-512 (1987); available from Stratagene, LaJolla, Calif.] is digested with BamHI and XhoI, made blunt-ended by treatment with the Klenow fragment of E. coli DNA polymerase, and the resulting 1.1 kb fragment is purified. pT164 is digested with BglII and made blunt-ended by treatment with the Klenow fragment of E. coli DNA polymerase. The two preceding blunt-ended fragments are ligated together and transformed into competent E. coli. Clones with a single insert of the 1.1 kb neo fragment are isolated and analyzed by restriction enzyme analysis to identify those in which the BglII site recreated by the fusion of the blunt XhoI and BglII sites is localized 1.3 kb away from the unique HindIII site present in plasmid pT164. The resulting plasmid, pT165, can now be cleaved at the unique BglII site flanking the 5' side of the neo transcription unit.

Detailed Description Text (111):
Oligonucleotides 13.8 and 13.9 are utilized in polymerase chain reactions to generate a fragment in which the mouse metallothionein I (mMT-I) promoter-hGH exon 1 sequences are additionally fused to a 10 base pair fragment comprising a splice donor site. The splice donor site chosen corresponds to the natural hEPO intron 1 splice donor site, although a larger number of splice donor sites or consensus splice donor sites can be used. The oligonucleotides (13.8 and 13.9) are used to amplify the approximately 0.73 kb mMT-I promoter-hGH exon 1 fragment from pXGH5 (FIG. 1). The amplified fragment (fragment 7) is digested with BglII and ligated to BglII digested pT165. The ligation mixture is transformed into E. coli and a clone, containing a single insert of fragment 7 in which the KpnI site in the mMT-I promoter is adjacent to the 5' end of the neo gene and the mMT-I promoter is oriented such that transcription is directed towards the unique HindIII site, is identified and designated pXEPO-12. ##STR3## The non-boldface region of oligo 13.8 is identical to the mMT-I promoter, with the natural KpnI site as its 5' boundary. The boldface type denotes a BglII site tail to convert the 5' boundary to a BglII site. ##STR4## The boldface region of oligos 13.9 denote hGH sequences. The italicized region corresponds to the first 10 base pairs of hEPO intron 1. The underlined BglII site is added for plasmid construction purposes.

Detailed Description Text (122):
A 0.2 kb DNA probe extending from the AccI site in hEPO exon 5 to the BglII site in the 3' untranslated region was used to probe RNA isolated from HT165-18A2-10 cells. The targeting construct, pXEPO-13, truncated at the AccI site in exon 5 does not contain these AccI/BglII sequences and, therefore, is diagnostic for targeting at the hEPO locus. Only cell strains that have recombined in a homologous manner with natural hEPO sequences would produce an hEPO mRNA containing sequence homologous to the AccI/BglII sequences. HT165-18A2-10 was found to express an mRNA of the predicted size hybridizing with the 32-P labeled AccI/BglII hEPO probe on Northern blots. Restriction enzyme and Southern blot analysis confirmed that the neo gene and mMT-I promoter were targeted to one of the two hEPO alleles in HT165-18A2-10 cells.

Other Reference Publication (7):
Rosenfeld, Melissa et al., "In Vivo Transfer of the Human Cystic Fibrosis Transmembrane Conductance Regulator Gene to the Airway Epithelium", Cell, 68:143-155 (1992).

Other Reference Publication (10):

Wolff, Jon A et al., "Direct Gene Transfer Into Mouse Muscle In Vivo", Science, 247:1465-1468 (1990).

Other Reference Publication (39):
Scharfmann, R., et al., "Long-Term In Vivo Expression of Retrovirus-Mediated Gene Transfer in Mouse Fibroblast Implants," Proc. Natl. Acad. Sci. USA, 88:4626-4630 (1991).

Other Reference Publication (40):
Wu, G.Y., "Receptor-Mediated Gene Delivery In Vivo," J. Biol. Chem., 266 (22):14338-14342 (1991).

CLAIMS:

45. A method of altering the expression of a targeted gene in a cell in vitro wherein the gene is not normally expressed in the cell, comprising the steps of:

(a) transfecting the cell in vitro with a DNA construct, the DNA construct comprising:

(i) a targeting sequence;

(ii) a regulatory sequence;

(iii) an exon; and

(iv) an unpaired splice donor site, thereby producing a transfected cell;and

(b) maintaining the transfected cell in vitro under conditions appropriate for homologous recombination, thereby producing a homologously recombinant cell; and

(c) maintaining the homologously recombinant cell in vitro under conditions appropriate for expression of the gene.

59. A method of making a protein by altering the expression of a targeted gene in a cell in vitro wherein the gene is not normally expressed in the cell, comprising the steps of:

a) transfecting the cell in vitro with a DNA construct, the DNA construct comprising:

(i) a targeting sequence;

(ii) a regulatory sequence;

(iii) an exon; and

(iv) an unpaired splice donor site, thereby producing a transfected cell;

(b) maintaining the transfected cell in vitro under conditions appropriate for homologous recombination, thereby producing a homologously recombinant cell; and

c) maintaining the homologously recombinant cell in vitro under conditions appropriate for expression of the gene thereby making the protein.

End of Result Set

☐ Generate Collection

L8: Entry 10 of 10 File: USPT Jun 24, 1997

DOCUMENT-IDENTIFIER: US 5641670 A
**** See image for Certificate of Correction ****
TITLE: Protein production and protein delivery

Brief Summary Text (12):
The invention further relates to a method of producing protein in vitro or in vivo through introduction of a construct as described above into host cell chromosomal DNA by homologous recombination to produce a homologously recombinant cell. The homologously recombinant cell is then maintained under conditions which will permit transcription, translation and secretion, resulting in production of the protein of interest.

Detailed Description Text (62):
In Vivo Protein Production

Detailed Description Text (85):
Gene targeting occurs when transfecting DNA either integrates into or partially replaces chromosomal DNA sequences through a homologous recombinant event. While such events can occur in the course of any given transfection experiment, they are usually masked by a vast excess of events in which plasmid DNA integrates by nonhomologous, or illegitimate, recombination.

Detailed Description Text (146):
Plasmid pXEPO-10 is designed to replace exon 1 of hEPO with exon 1 of hGH by gene targeting to the endogenous hEPO gene on human chromosome 7. Plasmid pXEPO-10 is constructed as follows. First, the intermediate plasmid pT163 is constructed by inserting the 6 kb HindIII-BamHI fragment (see Example 1f) lying upstream of the hEPO coding region into HindIII-BamHI digested pBluescriptII SK+ (Stratagene, LaJolla, Calif.). The product of this ligation is digested with XhoI and HindIII and ligated to the 1.1 kb HindIII-XhoI fragment from pMC1neoPolyA [Thomas, K. R. and Capecchi, M. R. Cell 51:503-512 (1987) available from Strategene, LaJolla, Calif.] to create pT163. Oligonucleotides 13.1-13.4 are utilized in polymerase chain reactions to generate a fusion fragment in which the mouse metallothionein 1 (mMT-I) promoter--hGH exon 1 sequences are additionally fused to hEPO intron 1 sequences. First, oligonucleotides 13.1 and 13.3 are used to amplify the approximately 0.73 kb mMT-I promoter--hGH exon 1 fragment from pXGH5 (FIG. 5). Next, oligonucleotides 13.2 and 13.4 are used to amplify the approximately 0.57 kb fragment comprised predominantly of hEPO intron 1 from human genomic DNA. Finally, the two amplified fragments are mixed and further amplified with oligonucleotides 13.1 and 13.4 to generate the final fusion fragment (fusion fragment 3) flanked by a SalI site at the 5' side of the mMT-I moiety and an XhoI site at the 3' side of the hEPO intron 1 sequence. Fusion fragment 3 is digested with XhoI and SalI and ligated to XhoI digested pT163. The ligation mixture is transformed into E. coli and a clone containing a single insert of fusion fragment 3 in which the XhoI site is regenerated at the 3' side of hEPO intron 1 sequences is identified and designated pXEPO-10. ##STR1## The non-boldface region of oligo 13.1 is identical to the mMT-I promoter, with the natural KpnI site as its 5' boundary. The boldface type denotes a SalI site tail to convert the 5' boundary to a SalI site. The boldface region of oligos 13.2 and 13.3 denote hGH sequences, while the non-boldface regions are intron 1 sequences from the hEPO gene. The non-boldface region of oligo 13.4 is identical to the last 25 bases of hEPO intron 1. The boldface region includes an XhoI site tail to convert the 3' boundary of the amplified fragment to an XhoI site.

Detailed Description Text (147):
Plasmid pXEPO-11 is designed to place, by gene targeting, the mMT-I promoter and exon

1 of hGH upstream of the hEPO structural gene and promoter region at the endogenous hEPO locus on human chromosome 7. Plasmid pXEPO-11 is constructed as follows. Oligonucleotides 13.1 and 13.5-13.7 are utilized in polymerase chain reactions to generate a fusion fragment in which the mouse metallothionein I (mMT-I) promoter--hGH exon 1 sequences are additionally fused to hEPO sequences from -1 to -630 relative to the hEPO coding region. First, oligonucleotides 13.1 and 13.6 are used to amplify the approximately 0.75 kb mMT-I promoter--hGH exon 1 fragment from pXGH5 (FIG. 5). Next, oligonucleotides 13.5 and 13.7 are used to amplify, from human genomic DNA, the approximately 0.65 kb fragment comprised predominantly of hEPO sequences from -1 to -620 relative to the hEPO coding region. Both oligos 13.5 and 13.6 contain a 10 bp linker sequence located at the hGH intron 1--hEPO promoter region, which corresponds to the natural hEPO intron 1 splice-donor site. Finally, the two amplified fragments are mixed and further amplified with oligonucleotides 13.1 and 13.7 to generate the final fusion fragment (fusion fragment 6) flanked by a SalI site at the 5' side of the mMT-I moiety and an XhoI site at the 3' side of the hEPO promoter region. Fusion fragment 6 is digested with XhoI and SalI and ligated to XhoI digested pT163. The ligation mixture is transformed into E. coli and a clone containing a single insert of fusion fragment 6 in which the XhoI site is regenerated at the 3' side of hEPO promoter sequences is identified and designated pXEPO-11. ##STR2## The boldface regions of oligos 13.5 and 13.6 denote hGH sequences. The italicized regions correspond to the first 10 base pairs of hEPO intron 1. The remainder of the oligos correspond to hEPO sequences from -620 to -597 relative to the hEPO coding region. The non-boldface region of oligo 13.7 is identical to bases -1 to -24 relative to the hEPO coding region. The boldface region includes an XhoI site tail to convert the 3' boundary of the amplified fragment to an XhoI site.

Detailed Description Text (151):
First, the intermediate plasmid pT164 is constructed by inserting the 6 kb HindIII-BamHI fragment (Example 1f) lying upstream of the hEPO coding region into HindIII-BamHI digested pBluescriptII SK+ (Stratagene, LaJolla, Calif.). Plasmid pMC1neoPolyA [Thomas, K. R. and Capecchi, M. R. Cell 51:503-512 (1987); available from Stratagene, LaJolla, Calif.] is digested with BamHI and XhoI, made blunt-ended by treatment with the Klenow fragment of E. coli DNA polymerase, and the resulting 1.1 kb fragment is purified. pT164 is digested with BglII and made blunt-ended by treatment with the Klenow fragment of E. coli DNA polymerase. The two preceding blunt-ended fragments are ligated together and transformed into competent E. coli. Clones with a single insert of the 1.1 kb neo fragment are isolated and analyzed by restriction enzyme analysis to identify those in which the BglII site recreated by the fusion of the blunt XhoI and BglII sites is localized 1.3 kb away from the unique HindIII site present in plasmid pT164. The resulting plasmid, pT165, can now be cleaved at the unique BglII site flanking the 5' side of the neo transcription unit.

Detailed Description Text (152):
Oligonucleotides 13.8 and 13.9 are utilized in polymerase chain reactions to generate a fragment in which the mouse metallothionein I (mMT-I) promoter--hGH exon 1 sequences are additionally fused to a 10 base pair fragment comprising a splice-donor site. The splice-donor site chosen corresponds to the natural hEPO intron 1 splice-donor site, although a larger number of splice-donor sites or consensus splice-donor sites can be used. The oligonucleotides (13.8 and 13.9) are used to amplify the approximately 0.73 kb mMT-I promoter--hGH exon 1 fragment from pXGH5 (FIG. 5). The amplified fragment (fragment 7) is digested with BglII and ligated to BglII digested pT165. The ligation mixture is transformed into E. coli and a clone, containing a single insert of fragment 7 in which the KpnI site in the mMT-I promoter is adjacent to the 5' end of the neo gene and the mMT-I promoter is oriented such that transcription is directed towards the unique HindIII site, is identified and designated pXEPO-12. ##STR3## The non-boldface region of oligo 13.8 is identical to the mMT-I promoter, with the natural KpnI site as its 5' boundary. The boldface type denotes a BglII site tail to convert the 5' boundary to a BglII site. ##STR4## The boldface region of oligos 13.9 denote hGH sequences. The italicized region corresponds to the first 10 base pairs of hEPO intron 1. The underlined BglII site is added for plasmid construction purposes.

Detailed Description Text (161):
A 0.2 kb DNA probe extending from the AccI site in hEPO exon 5 to the BglII site in the 3' untranslated region was used to probe RNA isolated from HT165-18A2-10 cells. The targeting construct, pXEPO-13, truncated at the AccI site in exon 5 does not

contain these AccI/BglII sequences and, therefore, is diagnostic for targeting at the hEPO locus. Only cell strains that have recombined in a homologous manner with natural hEPO sequences would produce an hEPO mRNA containing sequence homologous to the AccI/BglII sequences. HT165-18A2-10 was found to express an mRNA of the predicted size hybridizing with the 32-P labeled AccI/BglII hEPO probe on Northern blots. Restriction enzyme and Southern blot analysis confirmed that the neo gene and mMT-I promoter were targeted to one of the two hEPO alleles in HT165-18A2-10 cells.

Other Reference Publication (6):
Rosenfeld, Melissa A. et al., "In Vivo Transfer of the Human Cystic Fibrosis Transmembrane Conductance Regulator Gene to the Airway Epithelium," Cell 68:143-155 (1992).

Other Reference Publication (9):
Wolff, Jon A. et al., "Direct Gene Transfer into Mouse Muscle In Vivo," Science 247:1465-1468 (1990).

Other Reference Publication (36):
Scharfmann, R. et al., "Long-Term In Vivo Expression of Retrovirus-Mediated Gene Transfer in Mouse Fibroblast Implants," Proc. Natl. Acad. Sci. USA 88:4626-4630 (1991).

Other Reference Publication (37):
Wu, G.Y., "Receptor-Mediated Gene Delivery In Vivo," The Journal of Biological Chemistry 266(22):14338-14342 (1991).

09/245,549

ILE 'HOME' ENTERED AT 13:43:56 ON 02 JUL 2003

=> file caplus medline biosis embase
COST IN U.S. DOLLARS

	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	0.21	0.21

FILE 'CAPLUS' ENTERED AT 13:44:17 ON 02 JUL 2003
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FILE 'BIOSIS' ENTERED AT 13:44:17 ON 02 JUL 2003

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L1 0 HOMOLOG### (10A) RECOMGIN###(10A)(ONE INSERT OR SINGLE INSERT OR SINGLE DNA MOLECULE)

=> s homolog### (10a) recombin###(10a)(one insert or single insert or single DNA molecule)
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L4 ANSWER 1 OF 3 MEDLINE
AN 96355871 MEDLINE
DN 96355871 PubMed ID: 8751909
TI Porphyromonas gingivalis genes isolated by screening for epithelial cell attachment.
AU Duncan M J; Emory S A; Almira E C
CS Department of Molecular Genetics, Forsyth Dental Center, Boston, Massachusetts 02115, USA.
SO INFECTION AND IMMUNITY, (1996 Sep) 64 (9) 3624-31.
Journal code: 0246127. ISSN: 0019-9567.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-U60208
EM 199610
ED Entered STN: 19961015
Last Updated on STN: 19961015
Entered Medline: 19961003
AB Porphyromonas gingivalis is associated with chronic and severe periodontitis in adults. P. gingivalis and the other periodontal pathogens colonize and interact with gingival epithelial cells, but the genes and molecular mechanisms involved are unknown. To dissect the first

steps in these interactions, a P. gingivalis expression library was screened for clones which bound human oral epithelial cells. Insert DNA from the **recombinant** clones did not contain **homology** to the P. gingivalis fimA gene, encoding fimbrillin, the subunit protein of fimbriae, but showed various degrees of homology to certain cysteine protease-hemagglutinin genes. The DNA sequence of **one** **insert** revealed three putative open reading frames which appeared to be in an operon. The relationship between P. gingivalis attachment to epithelial cells and the activities identified by the screen is discussed.

AB . . . interactions, a P. gingivalis expression library was screened for clones which bound human oral epithelial cells. Insert DNA from the **recombinant** clones did not contain **homology** to the P. gingivalis fimA gene, encoding fimbrillin, the subunit protein of fimbriae, but showed various degrees of homology to certain cysteine protease-hemagglutinin genes. The DNA sequence of **one** **insert** revealed three putative open reading frames which appeared to be in an operon. The relationship between P. gingivalis attachment to. . .

L4 ANSWER 2 OF 3 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 1996:461581 BIOSIS
DN PREV199699183937
TI Porphyromonas gingivalis genes isolated by screening for epithelial cell attachment.
AU Duncan, M. J. (1); Emory, S. A.; Almira, E. C.
CS (1) Dep. Mol. Genet., Forsyth Dent. Cent., Boston, MA 02115 USA
SO Infection and Immunity, (1996) Vol. 64, No. 9, pp. 3624-3631. ISSN: 0019-9567.
DT Article
LA English
AB Porphyromonas gingivalis is associated with chronic and severe periodontitis in adults. P. gingivalis and the other periodontal pathogens colonize and interact with gingival epithelial cells, but the genes and molecular mechanisms involved are unknown. To dissect the first steps in these interactions, a P. gingivalis expression library was screened for clones which bound human oral epithelial cells. Insert DNA from the **recombinant** clones did not contain **homology** to the P. gingivalis fimA gene, encoding fimbrillin, the subunit protein of fimbriae, but showed various degrees of homology to certain cysteine protease-hemagglutinin genes. The DNA sequence of **one** **insert** revealed three putative open reading frames which appeared to be in an operon. The relationship between P. gingivalis attachment to epithelial cells and the activities identified by the screen is discussed.

AB. . . interactions, a P. gingivalis expression library was screened for clones which bound human oral epithelial cells. Insert DNA from the **recombinant** clones did not contain **homology** to the P. gingivalis fimA gene, encoding fimbrillin, the subunit protein of fimbriae, but showed various degrees of homology to certain cysteine protease-hemagglutinin genes. The DNA sequence of **one** **insert** revealed three putative open reading frames which appeared to be in an operon. The relationship between P. gingivalis attachment to. . .

L4 ANSWER 3 OF 3 EMBASE COPYRIGHT 2003 ELSEVIER SCI. B.V.
AN 96276489 EMBASE
DN 1996276489
TI Porphyromonas gingivalis genes isolated by screening for epithelial cell attachment.
AU Duncan M.J.; Emory S.A.; Almira E.C.
CS Department of Molecular Genetics, Forsyth Dental Center,Boston, MA 02115, United States
SO Infection and Immunity, (1996) 64/9 (3624-3631). ISSN: 0019-9567 CODEN: INFIBR
CY United States

DT Journal; Article
FS 004 Microbiology
LA English
SL English
AB Porphyromonas gingivalis is associated with chronic and severe periodontitis in adults. P. gingivalis and the other periodontal pathogens colonize and interact with gingival epithelial cells, but the genes and molecular mechanisms involved are unknown. To dissect the first steps in these interactions, a P. gingivalis expression library was screened for clones which bound human oral epithelial cells. Insert DNA from the **recombinant** clones did not contain **homology** to the P. gingivalis fimA gene, encoding fimbrillin, the subunit protein of fimbriae, but showed various degrees of homology to certain cysteine protease-hemagglutinin genes. The DNA sequence of **one insert** revealed three putative open reading frames which appeared to be in an operon. The relationship between P. gingivalis attachment to epithelial cells and the activities identified by the screen is discussed.
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